

HIV1LAI (DP-178; SEQ ID:1)	YTSLIHSLIEESQNQQEKNEQELLELDKWA SLWNMF
HIV1SF2 (DP-185; SEQ ID:3)	YTNTIYNLLESQNQQEKNEQELLELDKWA SLWNMF
HIV1RF (SEQ ID:4)	YTGIYNLLESQNQQEKNEQELLELDKWA NLWNMF
HIV1MN (SEQ ID:5)	YTSLIYSLLEKSQTQ&EKNQELLELDKWA SLWNMF
HIV2ROD (SEQ ID:6)	LEANISKSLE Q AQIQQEK N MYELQ K LN S W I FGNMF
HIV2NIHZ (SEQ ID:7)	LEANISQSLE Q QIQQEK N MYELQ K LN S W I VFTNWL
DP180 (SEQ ID:2)	SSESSFTLLEQW W WKLQLAEQ W LEQINEKHYLEDIS
DP118 (SEQ ID:10)	QQLLDWVKRQQEMRLT W CTKNLQARVTAIEKYLKDQ
DP125 (SEQ ID:8)	CGGNILLRAIEAQQHLQLQ W IKQLQARILAVERYLKDQ
DP116 (SEQ ID:9)	LQARILAVERYLKDQQQ

FIG. 1

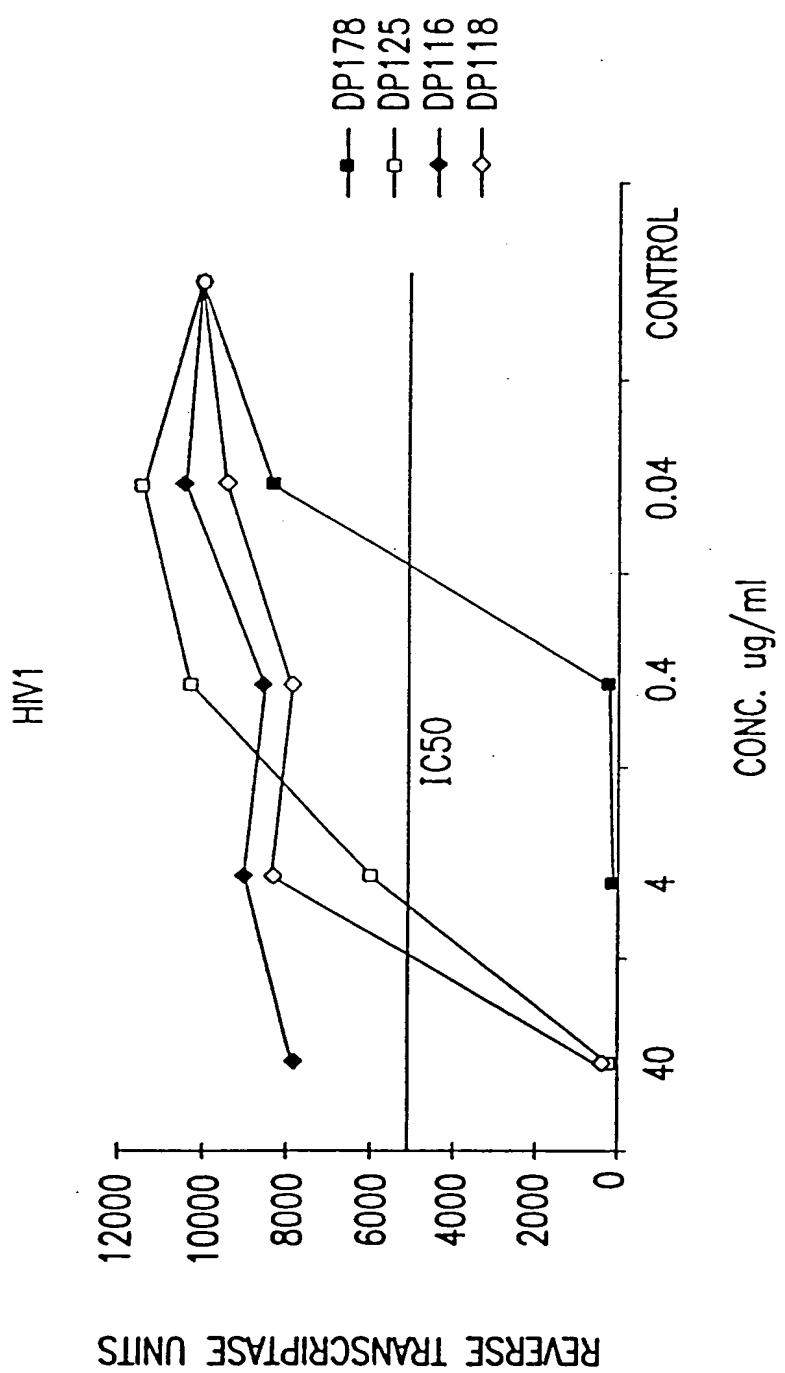


FIG. 2

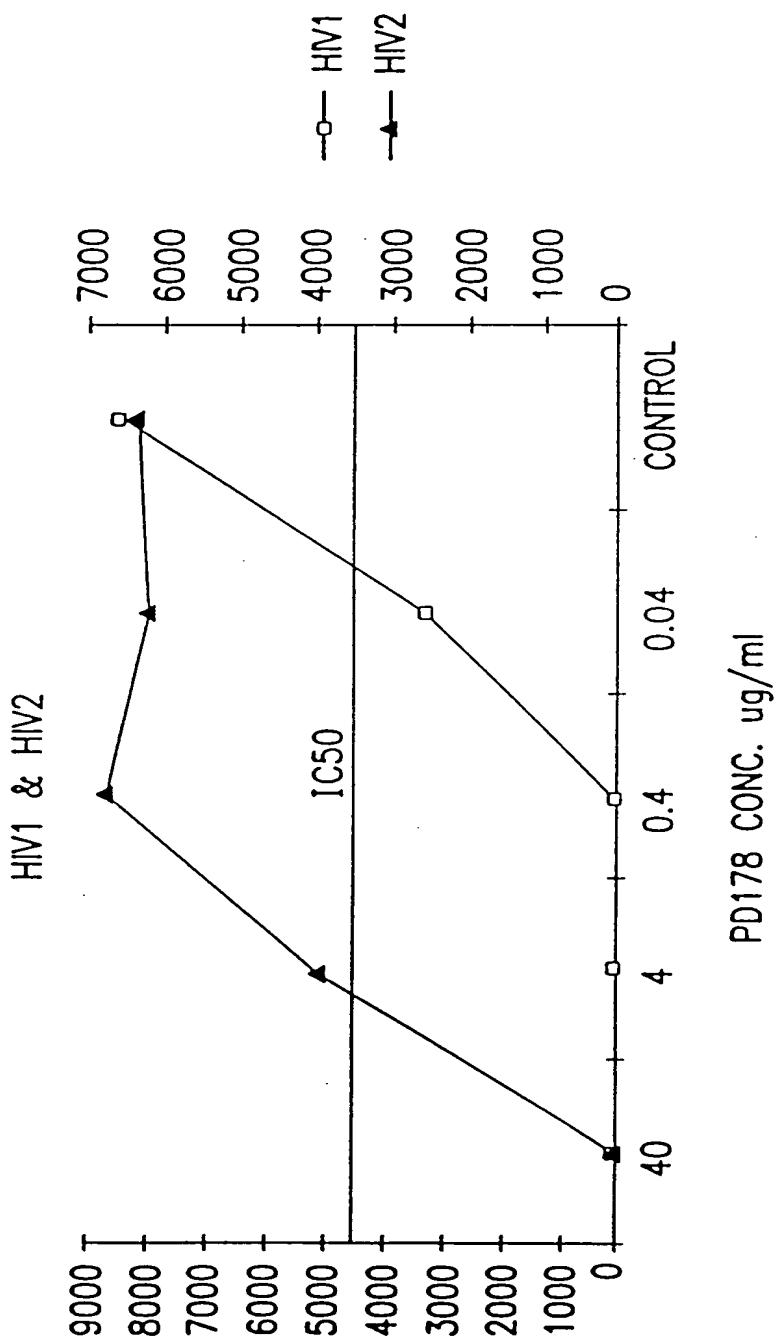


FIG. 3

Number of Syncytia/well: concentration in $\mu\text{g}/\text{ml}$ (micrograms/ml)									
DP178	10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
<i>Syncytia</i>									
HIV1LAI	0	0	0	0	0	0	0	0	67
HIV1MN	0	0	0	0	0	ND	ND	ND	34
HIV1RF	0	0	0	0	0	ND	ND	ND	65
HIV1SF2	0	0	0	0	0	ND	ND	ND	58
DP125	10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
<i>Syncytia</i>									
HIV1LAI	0	0	54	69	80	75	79	82	67
HIV1MN	0	0	30	36	ND	ND	ND	ND	34
HIV1RF	0	0	67	63	ND	ND	ND	ND	65
HIV1SF2	0	0	9	66	ND	ND	ND	ND	58
DP116	10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
<i>Syncytia</i>									
HIV1LAI	75	ND	ND	ND	ND	ND	ND	ND	67
HIV1MN	35	ND	ND	ND	ND	ND	ND	ND	34
HIV1RF	81	ND	ND	ND	ND	ND	ND	ND	65
HIV1SF2	81	ND	ND	ND	ND	ND	ND	ND	58

FIG.4A

DP180	40	20	10	5	2.5	1.25	0.625	0.3125	Control
<i>Syncytia</i>									
HIV1LAI	50	>45	>45	>45	>45	>45	>45	>45	58
DP185	40	20	10	5	2.5	1.25	0.625	0.3125	Control
<i>Syncytia</i>									
HIV1LAI	0	0	0	0	0	0	0	ND	60

FIG.4B

HIV1Number of Syncytia/well: concentration in ng/ml (nanograms/ml)

DP178	20	10	5	2.5	1.25	0.625	0.3125	Control
<u>Syncytia</u>								
HIV1	0	0	0	0	0	14	20	48
<u>DP116</u>								
Syncytia	20	10	5	2.5	1.25	0.625	0.3125	Control
HIV1	ND	48	ND	ND	ND	ND	ND	ND

HIV2Number of Syncytia/well: concentration in μ g/ml (micrograms/ml)

DP178	20	10	5	2.5	1.25	0.625	0.3125	Control
<u>Syncytia</u>								
HIV2	50	54	55	57	63	77	78	76
<u>DP116</u>								
Syncytia	20	10	5	2.5	1.25	0.625	0.3125	Control
HIV2	ND	58	ND	ND	ND	ND	ND	ND

FIG.5

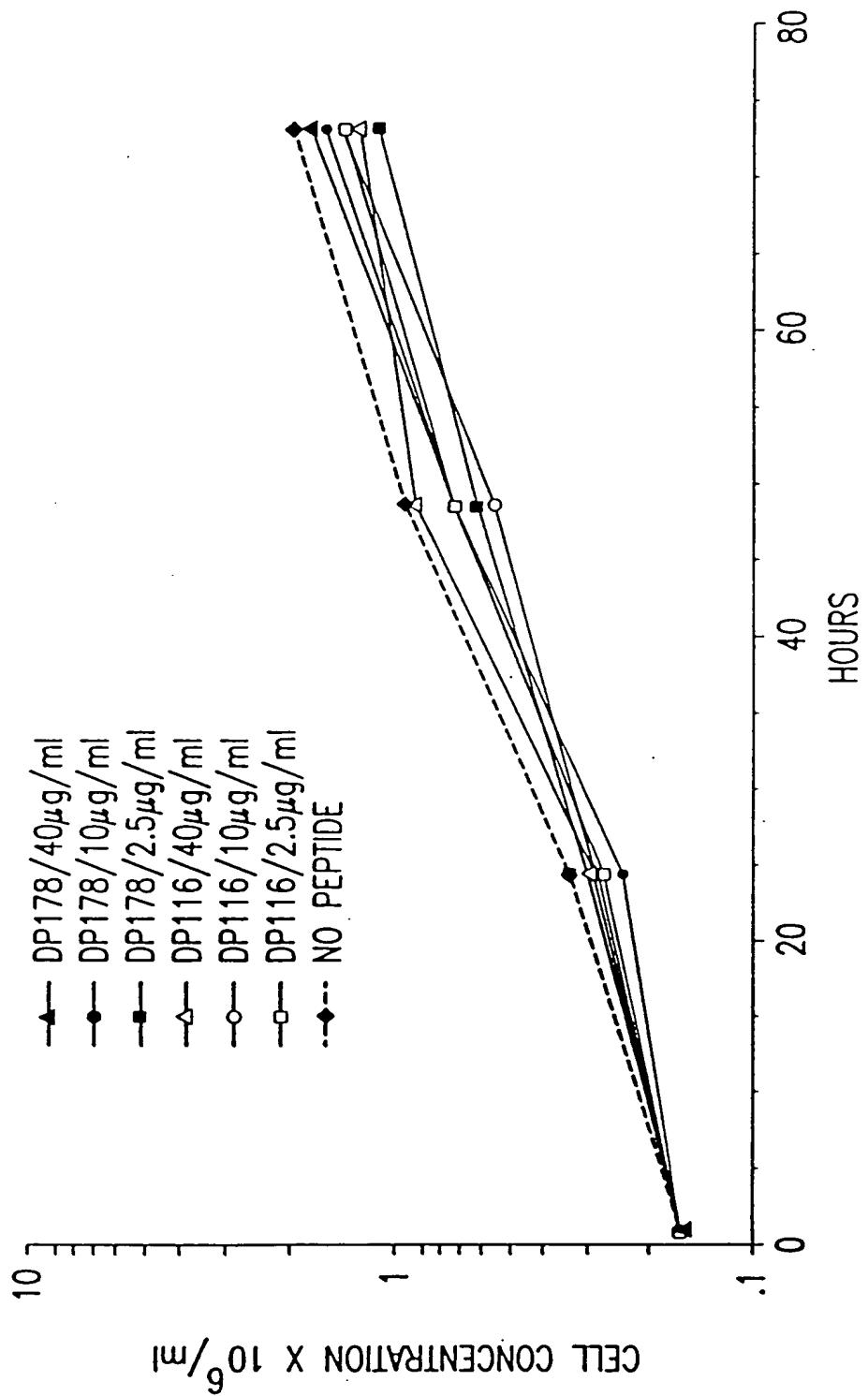


FIG. 6

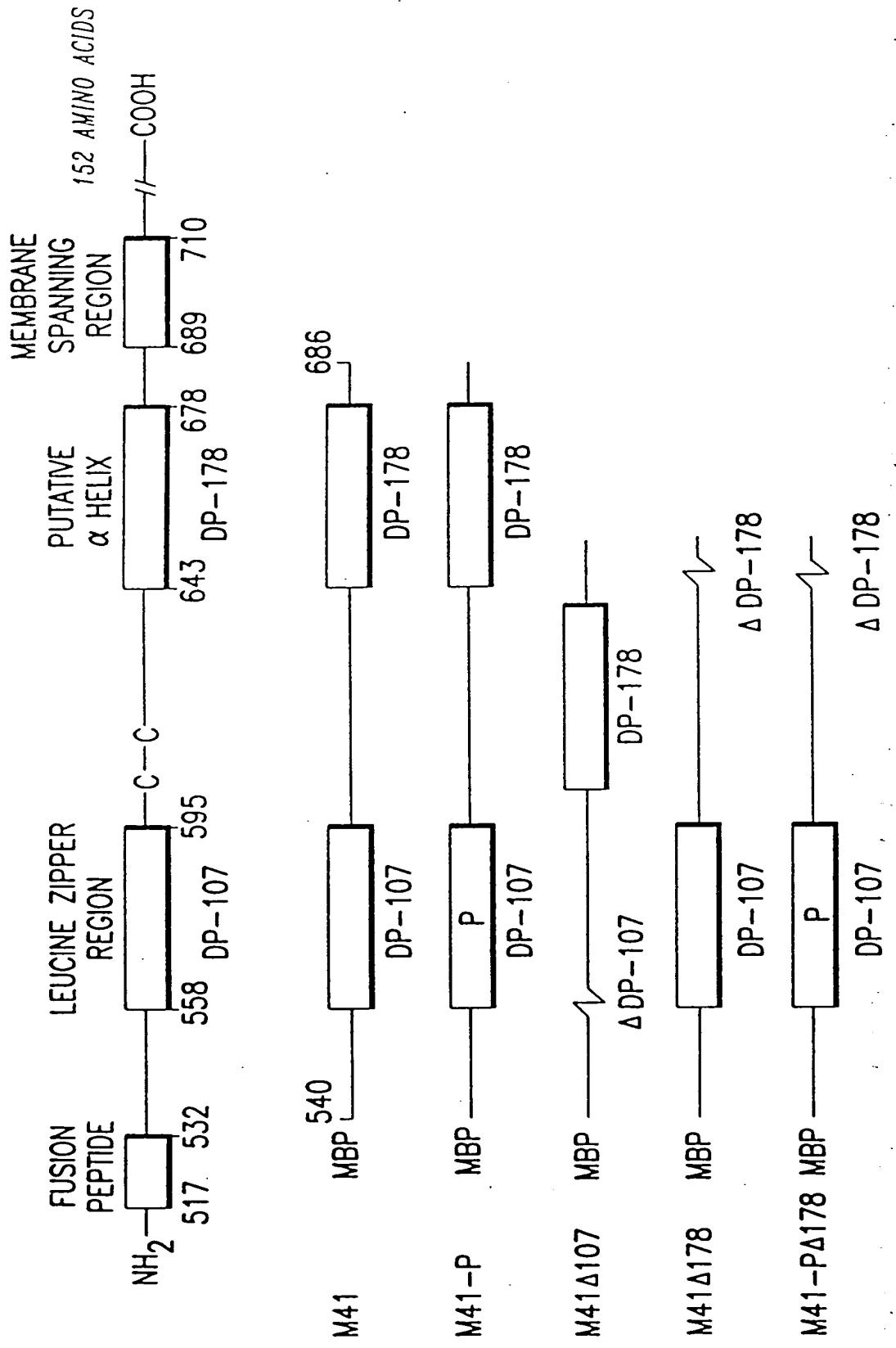


FIG. 7

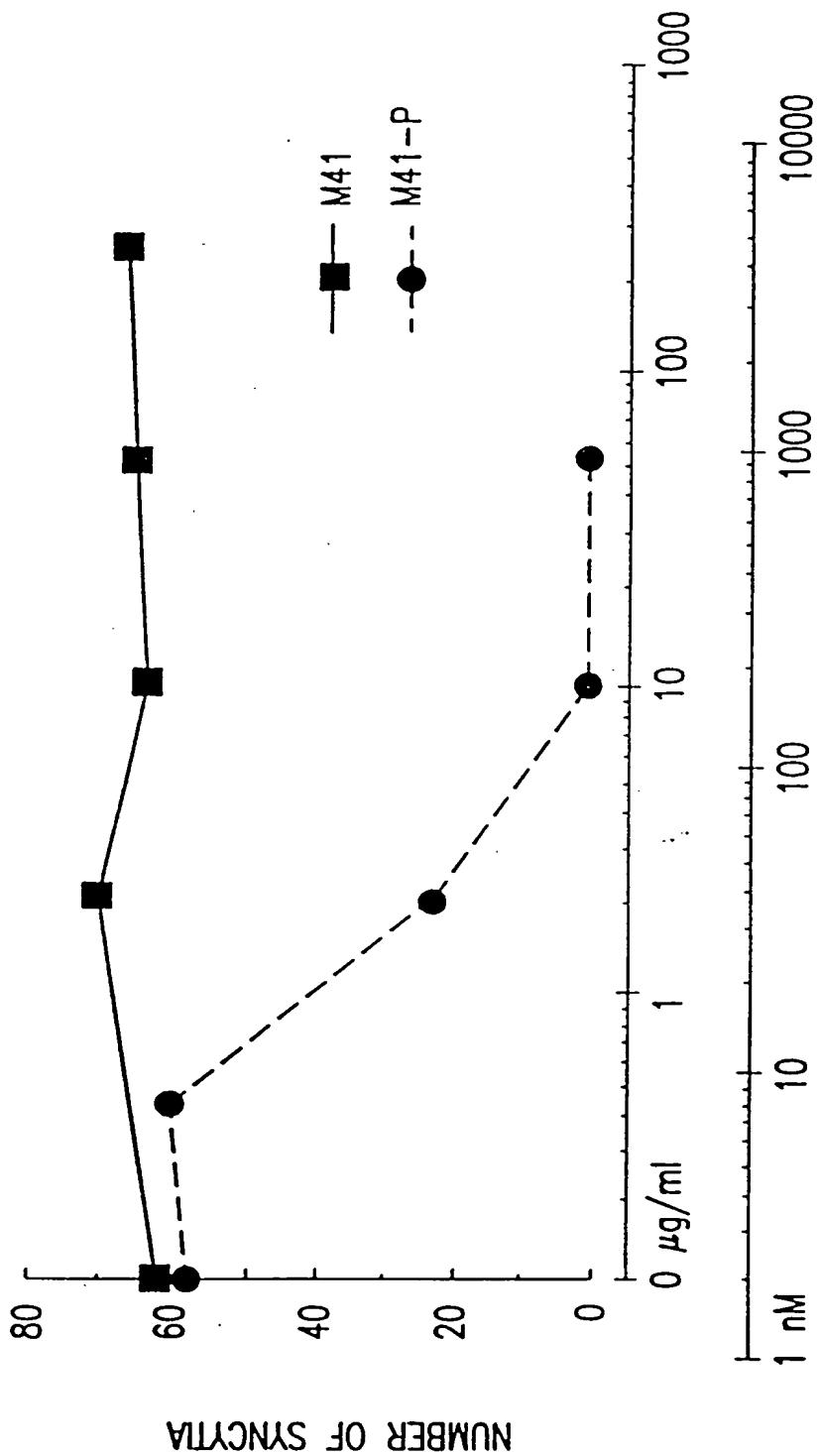


FIG.8

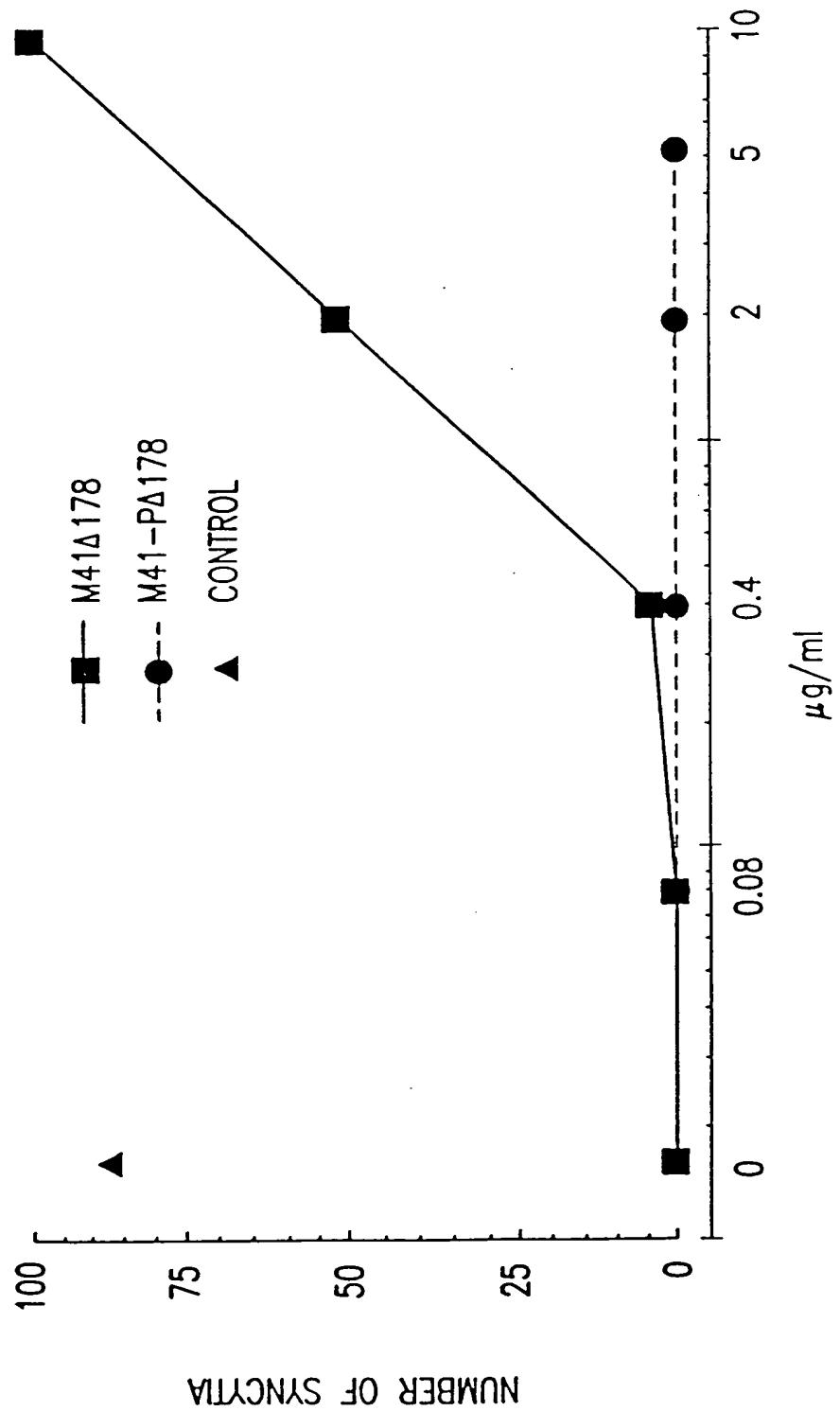


FIG. 9

08/487355

7872-020 (SHEET 10 OF 63)

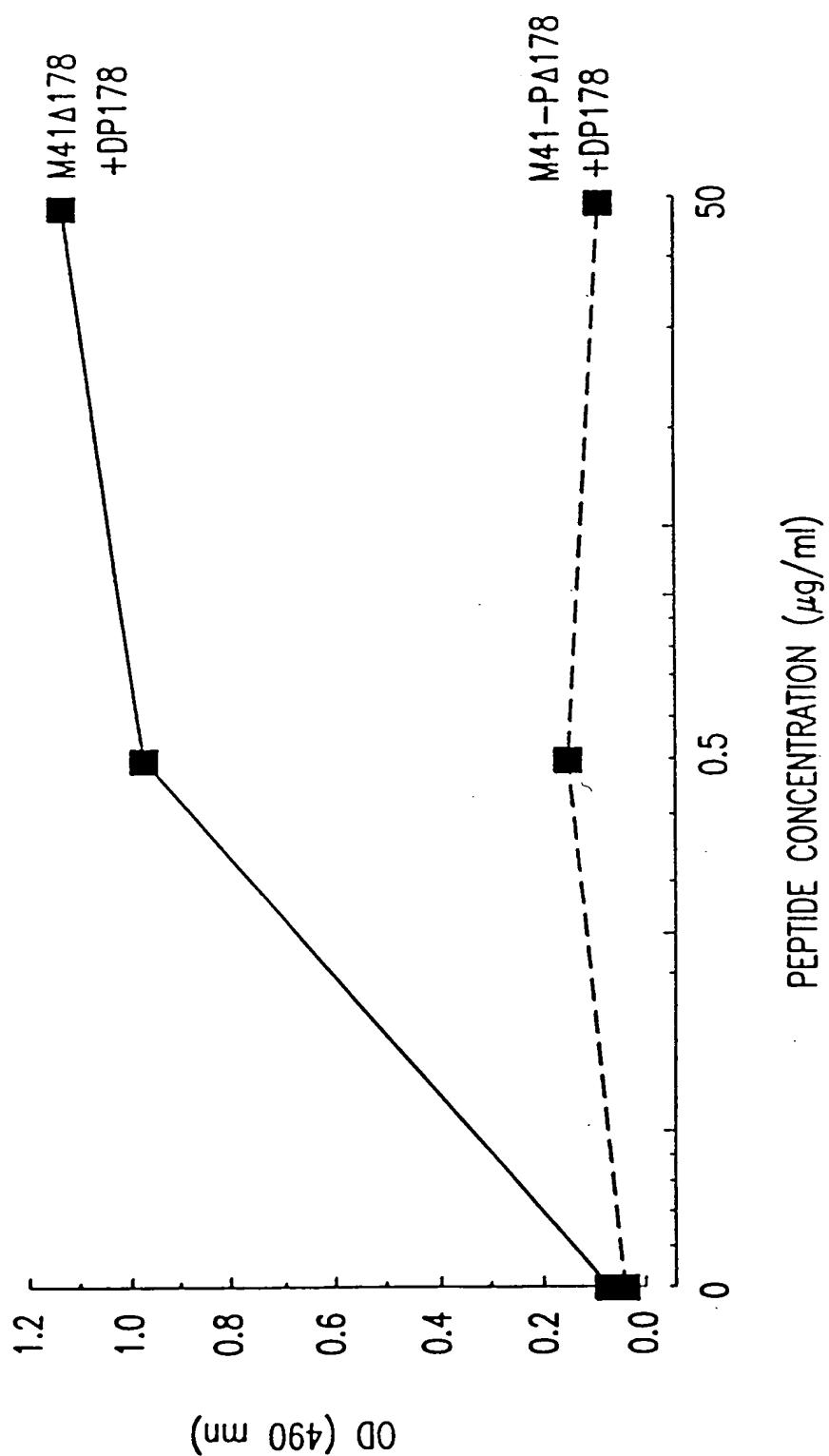


FIG. 10

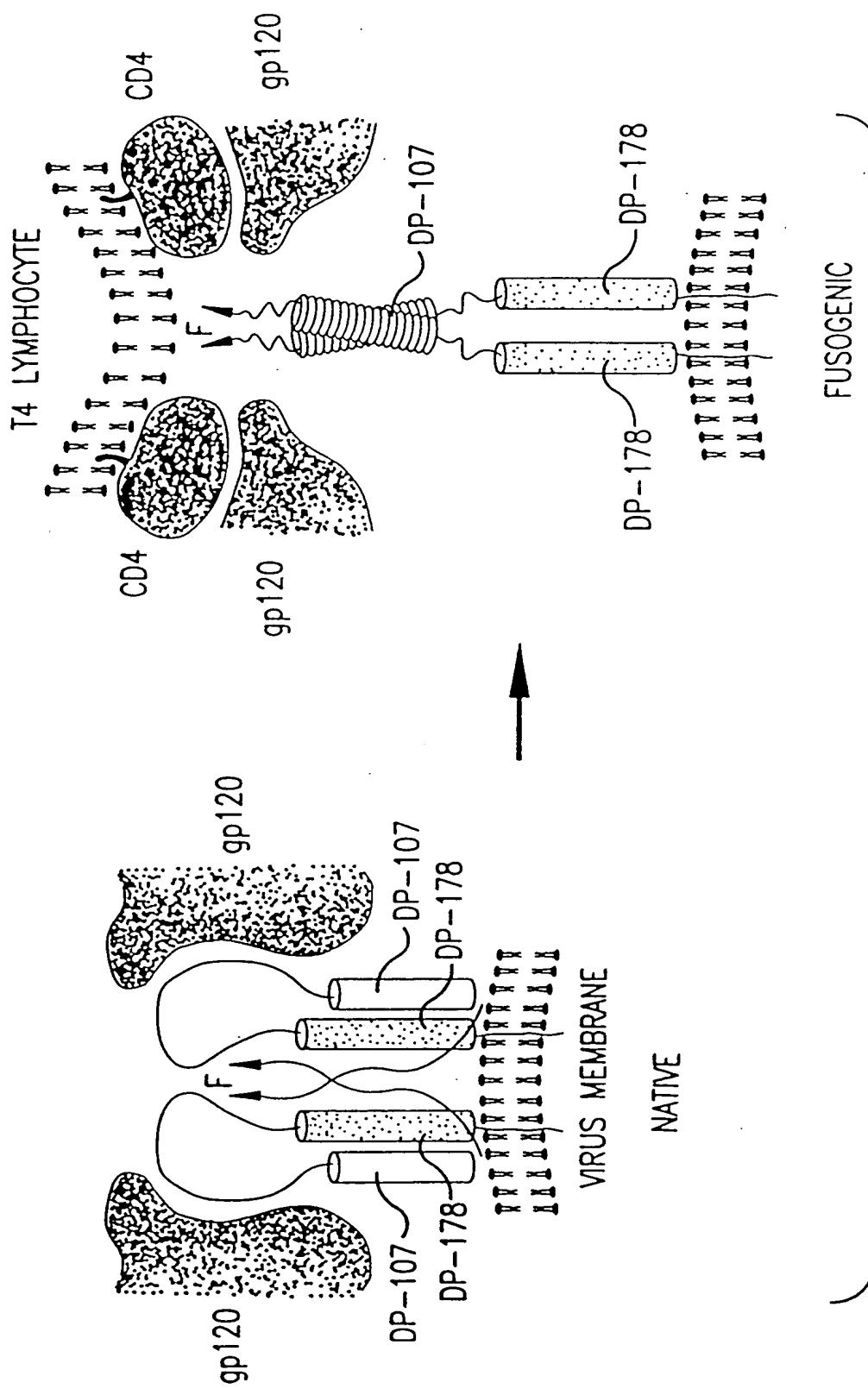


FIG. 11A

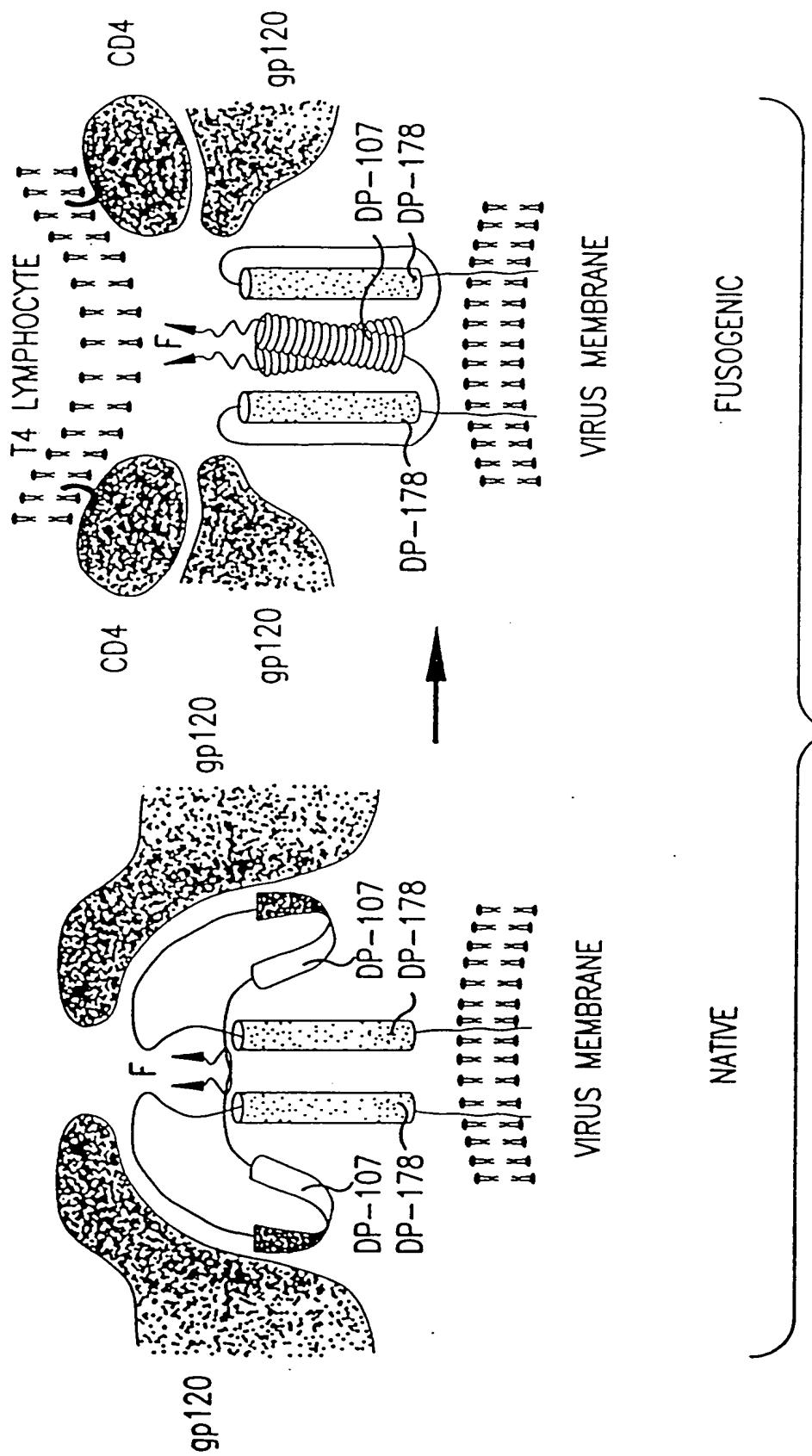


FIG. 11B

Sequence	Positions								Motifs
	A	D	A	D	A	D	A	D	
GCN4 (gcn4 yeast)	W	K	Q	L	E	D	K	V	[LMNV] {CFGIMPWTW}
C-FOS (fos_human)	T	D	T	L	Q	A	E	T	[IKL] {CFGHIIMPWVWY}
C-JUN (c-jun_human)	I	A	R	L	E	K	V	K	[AILN] {CDFGHILPWWY}
C-MYC (myo_human)	E	Q	K	L	I	S	E	E	[ELR] {ACFGIMPWWY}
FLU LOOP 36	I	E	K	T	N	E	K	F	[FILTV] {ACFLMPTWW}

FIG.12

Sequence	Positions												Motifs				
DP-107 (env_hv1bru) L1=0	N	N	L	R	A	Q	H	L	L	Q	T	V	W	G	D	{LQT}	{CFIMPSTY}
DP-107 (env_hv1bru) L1=0	N	N	L	R	A	Q	H	L	L	Q	T	V	W	G	A	{LQT}	{CDFIMPST}
DP-107 (env_hv1bru) L1=0	N	N	L	R	A	Q	H	L	L	Q	T	V	W	G	D	{LQT}	{CDFIMPST}
DP-107 (env_hv1bru) L2=0	N	N	L	L	R	A	I	E	A	Q	Q	H	L	L	A	{EKLNOV}	{CDFKMPSY}
DP-107 (env_hv1bru) L2=0	N	N	L	L	R	A	I	E	A	Q	Q	H	L	L	D	{EKLNOV}	{CDFKMPSY}
DP-107 (env_hv1bru) L2=0	N	N	L	L	R	A	I	E	A	Q	Q	H	L	L	A	{EKLNOV}	{CDFKMPSY}
DP-107 (env_hv1bru) L2=0	N	N	L	L	R	A	I	E	A	Q	Q	H	L	L	D	{EKLNOV}	{CDFKMPSY}
DP-178 (env_hv1bru) Y1=A	Y	T	S	L	I	H	S	L	I	E	S	Q	N	E	K	{EKLQXY}	{ACFGMPRWY}
DP-178 (env_hv1bru) Y1=A	Y	T	S	L	I	H	S	L	I	E	S	Q	N	E	K	{EKLQXY}	{ACFGMPRWY}
DP-178 (env_hv1bru) Y1=A	Y	T	S	L	I	H	S	L	I	E	S	Q	N	E	K	{EKLQXY}	{ACFGMPRWY}
DP-178 (env_hv1bru) Y1=A	Y	T	S	L	I	H	S	L	I	E	S	Q	N	E	K	{EKLQXY}	{ACFGMPRWY}
DP-178 (env_hv1bru) Y1=D	Y	T	S	L	I	H	S	L	I	E	S	Q	N	E	K	{EILNOQSY}	{ACFGMPRWY}
DP-178 (env_hv1bru) Y1=D	Y	T	S	L	I	H	S	L	I	E	S	Q	N	E	K	{EILNOQSY}	{ACFGMPRWY}
DP-178 (env_hv1bru) Y1=D	Y	T	S	L	I	H	S	L	I	E	S	Q	N	E	K	{EILNOQSY}	{ACFGMPRWY}
DP-178 (env_hv1bru) Y1=D	Y	T	S	L	I	H	S	L	I	E	S	Q	N	E	K	{EILNOQSY}	{ACFGMPRWY}

FIG. 13

FIG. 14

Sequence	Positions										Parent Motif	Hybrid Motif																	
	D	A	D	A	D	A	D	A	D	A																			
GCN4 (gen4 yeast)	W	K	Q	L	E	D	K	V	E	L	S	K	N	Y	H	L	E	N	V	A	R	L	K	K	L	[LMIV] {CFGIMPW}	[LMIV] {CFGIMPW}		
DP-178 (env_hv1bru) Y1=A	Y	T	SL	I	H	S	L	I	E	S	N	Q	E	K	N	Q	E	K	N	Q	E	K	N	Q	E	K	N	[EKLY] {ACFGPRWY}	[EKLY] {ACFGPRWY}
DP-178 (env_hv1bru) Y1=A	Y	T	SL	I	H	S	L	I	E	S	N	Q	E	K	N	Q	E	K	N	Q	E	K	N	Q	E	K	N	[EKLQWY] {CFGMP}	[EKLQWY] {CFGMP}
DP-178 (env_hv1bru) Y1=A	Y	T	SL	I	H	S	L	I	E	S	N	Q	E	K	N	Q	E	K	N	Q	E	K	N	Q	E	K	N	[EFLKQWY] {CFGMP}	[EFLKQWY] {CFGMP}
DP-178 (env_hv1bru) Y1=A	Y	T	SL	I	H	S	L	I	E	S	N	Q	E	K	N	Q	E	K	N	Q	E	K	N	Q	E	K	N	[EFLKQWY] {CFGMP}	[EFLKQWY] {CFGMP}
DP-178 (env_hv1bru) Y1=A	Y	T	SL	I	H	S	L	I	E	S	N	Q	E	K	N	Q	E	K	N	Q	E	K	N	Q	E	K	N	[EILNQSY] {ACFGMPWY}	[EILNQSY] {ACFGMPWY}
DP-178 (env_hv1bru) Y1=A	Y	T	SL	I	H	S	L	I	E	S	N	Q	E	K	N	Q	E	K	N	Q	E	K	N	Q	E	K	N	[EILNQSY] {CFGMPWY}	[EILNQSY] {CFGMPWY}
DP-178 (env_hv1bru) Y1=A	Y	T	SL	I	H	S	L	I	E	S	N	Q	E	K	N	Q	E	K	N	Q	E	K	N	Q	E	K	N	[EILNQSY] {CFGMPWY}	[EILNQSY] {CFGMPWY}
DP-178 (env_hv1bru) Y1=A	Y	T	SL	I	H	S	L	I	E	S	N	Q	E	K	N	Q	E	K	N	Q	E	K	N	Q	E	K	N	[EFLILNQSY] {CFGMPWY}	[EFLILNQSY] {CFGMPWY}
DP-178 (env_hv1bru) Y1=A	Y	T	SL	I	H	S	L	I	E	S	N	Q	E	K	N	Q	E	K	N	Q	E	K	N	Q	E	K	N	[EFLILNQSY] {CFGMPWY}	[EFLILNQSY] {CFGMPWY}

FIG. 15

Sequence	Positions				Parent Motif				Hybrid Motif			
	A	D	A	D	A	D	A	D	A	D	A	D
DP-107 (env_hv1bru) Y1=D	N	N	R	A	Q	H	L	Q	T	W	G	I
DP-107 (env_hv1bru) Y2=D	N	N	R	A	Q	H	L	Q	T	W	G	I
DP-178 (env_hv1bru) Y1=A	Y	T	S	L	I	H	S	L	E	S	N	Q
DP-178 (env_hv1bru) Y1=D	Y	T	S	L	I	H	S	L	E	S	N	Q
FLU LOOP 36	I	E	K	T	N	E	K	F	H	Q	I	E

FIG.16

Sequence	Positions				Parent Motif	Hybrid Motif
	A	D	A	D		
GCN4 (gcn4 yeast)	W	K	Q	I	EDKVEEL	[LAVRILKKL]
DP-107 (env_hv1bry) L1=0	N	N	L	R	QHLLQQLTYWG	[LQTV] {CQFIMPSTI}
DP-178 (env_hv1bry) Y1=A	Y	T	S	L	IEAQSQQEKLQ	[EFKLQWY] {CFCGPRVY}
GCN4 (gcn4 yeast)	W	K	Q	I	EDKVEEL	[LAVRILKKL]
DP-107 (env_hv1bry) L1=0	N	N	L	R	QHLLQQLTYWG	[LQTV] {CQFIMPSTI}
DP-178 (env_hv1bry) Y1=A	Y	T	S	L	IEEESQNLQEQE	[EFILNQSYWY] {CFCGPRVY}
GCN4 (gcn4 yeast)	W	K	Q	I	EDKVEEL	[LAVRILKKL]
DP-107 (env_hv1bry) L2=0	N	N	L	R	QHLLQQLTYWG	[LQTV] {CQFIMPSTI}
DP-178 (env_hv1bry) Y1=A	Y	T	S	L	IEEESQNLQEQE	[EFILNQSYWY] {CFCGPRVY}
GCN4 (gcn4 yeast)	W	K	Q	I	EDKVEEL	[LAVRILKKL]
DP-107 (env_hv1bry) L2=0	N	N	L	R	QHLLQQLTYWG	[LQTV] {CQFIMPSTI}
DP-178 (env_hv1bry) Y1=A	Y	T	S	L	IEEESQNLQEQE	[EFILNQSYWY] {CFCGPRVY}

FIG. 17

Sequence	Positions				Parent Motif	Hybrid Motif
	D	A	D	A		
GCN4 (gcn4 yeast)	W K Q L E D K V E E L L S K N Y H L E N E V A R L K K L	N N L L R A I E A Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q	[LMNV] {FCGIMPWT}	[LMNV] {FCGIMPWT}		
DP-107 (env_hvibr) Y1=D	W K Q L E D K V E E L L S K N Y H L E N E V A R L K K L	N N L L R A I E A Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q	[LMNV] {FCGIMPWT}	[LMNV] {FCGIMPWT}		
DP-107 (env_hvibr) Y2=D	W K Q L E D K V E E L L S K N Y H L E N E V A R L K K L	N N L L R A I E A Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q	[LMNV] {FCGIMPWT}	[LMNV] {FCGIMPWT}		
DP-178 (env_hvibr) Y1=A	W K Q L E D K V E E L L S K N Y H L E N E V A R L K K L	N N L L R A I E A Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q	[LMNV] {FCGIMPWT}	[LMNV] {FCGIMPWT}		
DP-178 (env_hvibr) Y1=D	W K Q L E D K V E E L L S K N Y H L E N E V A R L K K L	N N L L R A I E A Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q	[LMNV] {FCGIMPWT}	[LMNV] {FCGIMPWT}		
C-FOS (fos_human)	I D T I L Q A E I D Q L E D E K S A L Q T E I A N L L K E	I D T I L Q A E I D Q L E D E K S A L Q T E I A N L L K E	[IKL] {FCGHIMPWY}	[IKL] {FCGHIMPWY}		
C-JUN (top1_human)	I A R L E E K V K T L K A Q N S E L A S T A N W L R E Q	I A R L E E K V K T L K A Q N S E L A S T A N W L R E Q	[AILNV] {CDFGHILPWTY}	[AILNV] {CDFGHILPWTY}		
C-MYC (myo_human)	E Q K L I S E E D L L E K R R E Q L K H K L E Q L R N S	E Q K L I S E E D L L E K R R E Q L K H K L E Q L R N S	[ELR] {ACFGIMPWTY}	[ELR] {ACFGIMPWTY}		
FLU LOOP 36	I E K T N E K F H Q I E K F S E V E G R I I Q D L E K Y	I E K T N E K F H Q I E K F S E V E G R I I Q D L E K Y	[FLTV] {ACFLIMPWTY}	[FLTV] {ACFLIMPWTY}		

$$= \{CDGHP\} \{CFP\}$$

FIG. 18

FIG. 19

Fusion ♦ALLMOT15♦
 Peptide ♦107x178x4♦
 ♦.....ELGELG A AGSTMGARSM TLTQVQARQ ♦LL SGIVQQQ DPI07-NNL

LRAIEAOOHL LOLTVWGIKO LOARILAYER YLKDO-DPI07 QLLG♦♦ I WGC

♦107x178x4♦
 ♦ALLMOT15♦ *LVS Coiled-Coil*
 SGKLICT TAVP ♦WNASWS NKSLEQIWNN MTWM *E ♦WDREINN DPI78-

YTSLIHSL IEESONOOEK NEOELLELDK* WASLWNWF-DPI78 NI

♦Transmembrane Region♦
 TNWLWYIK♦ ♦IFIMIVGGGLVGLRIVFAVLSIV NRVHQGYS♦ PL

♦P23LZIPC♦
 SFQTHLPTPR GPDR ♦PEGIEE EGGERDRDRS IRLVNGSLAL IWDDLRSL♦ CL

♦ALLMOT15♦ ♦107x178x4♦
 F ♦SYHRLRDLL LIVTRIVELL GRRGW ♦EALKY WWNLLQXWSQ

ELKNSAVSLL NAT♦ AIAVAEG TDRVIEVVQG A♦ CRAIRHPR

RIRQGLERIL L

FIG. 20

Fusion ♦ALLMOT15♦
 Peptide ♦107x178x4♦
 ♦.....ELGEL LGVGSAIAS GVA ♦VSKVLHL EGEVN KIKSA

♦P1&12LZIPC♦
LLSTNKAVVS LSNGVSVLTS KVLDLKNYID KQ♦ ♦ LL ♦PIVNKQ♦
 ♦107x178x4♦
 SC ♦SISNIETVI+ EFQQKNNRLLEITREFSVNAG♦ VTIIPVSTMLTINSELLSL

♦P1&12LZIPC♦
 ♦ALLMOT15♦
 INDM ♦PI ♦TNDQ KKLMSSNNVQI V+ RQQSYSI+ MS IIKEEVLAYV

VQ♦ LPLYGVID TPCWKLHTSP LCTTNTKEGS NICLRTDRG WYCDNAGSVS

FFPQAETCKV QSNR VFCDTM NSLTPSEIN LCNVDIFNPK

YDCKIMTSKT DVSSSVITSL GAIVSCYGKT KCTASNKNRG

IIKTFNGCDYVSNKGMDTV SVGNTLYYVN KQEGKSLYVK G

♦P7, 12, & 23LZIPC♦
 ♦107x178x4♦ ♦ALLMOT15♦
 EPIINFYDPLVF ♦PSDE ♦EDASISQVNEKINOSLAF ♦I+ RKSDELL+

♦ Transmembrane Region ♦
HNVNA♦ GK STTN ♦IMITIIVIVIVILLS LIAVGLLLY♦ C♦

KARSTPVTLS KDQLSGINNI AFSN

Fusion
 Peptide **ALLMOTIS** **107x178x4**
 **FLGELG** **AAGTA MGAAA** **TALTYOSQHLLAGILQQOKNLLAAV**

EAQ **QQM** **107x178x4** **LKLTIWGYKNLNARYTALEKYLEDQARLN** **AWG** **CA**

LVS Coiled-Coil
ALLMOTIS **107x178x4**
WKQVCHTTVP **WQWNNRTPDW** **NNMT** **WLE** **WERQISYLEGNIT**

TQLEEARAQEEKNLD **AYQKLSS** **WSDFWSW** **FDF** **107x178x4** **SKWLN** **ILK**

♦ Transmembrane Region ♦
IGFLDYLGNGLRLLYTV ♦ **XS** ♦ **CIARVRQGYS** **PLSPQIHIHP** **WKGQPDNAEG**

PGEGGDKRKN **SSEPWQKESG** **TAEWKSNWCK** **RLTNWCSISS** **IWL** **YNS**

♦ **ALLMOTIS** ♦
 ♦ **CLTL** **LVHLRSAFQY** **IQYGLGELKA** **AAQEAVVALA** **RLAQNAGYQIWL** ♦

ACRSAYRA **IINSPRRVRQ** **GLEGILN**

FIG. 22

Fusion Peptide **▼ALLMOTIS▼** **↑107x178x4↑**
EAG **▼VVL** **AGVALGVATA AQITAGIALHQ** **↑*SNLNAQAIQ**
LVS Coiled-Coil

SLRTSLEQSNKAIEEIREATQETVIA* **VQGVQDY** **↑ VNNEV** **VP**

▼ALLMOTIS▼
↑107x178x4↑
+P6 & 12LZIPC+
AMQHMSCELVGQRLGLRLLRYYTELLSIFGPSLRD **↑PISA** **↑*EISIQALIYAL**

GGEIHKILEKLGYSGSD **↑ MIAILESRGIKTKI** **▼ THVDLPGKF IILSISY**

+P1 & 12LZIPC+
+PTLSEVKGVIVHRLEAV **↑ SYNIGSQEWYTTVPRYIATNGYLISNFDESSCVFVS**

ESAICSQNSL YPMSPPLLQQC IRGDTSSCAR TLVSGTMGNK FILSKGNIVA

NCASILCKCY STSTIINQSP DKLLTFLASD TCPLVEIDGA TIQVGGRQYP

LVS Coiled-Coil
▼ALLMOTIS▼
+P12 & 23LZIPC+
DMVYEGKVAL G **↑PAISLD** **▼RL*DYGTNLGNALKLDDAKVLI+**

♦ Transmembrane Region ♦
DSS **↑NQILETYR RS** **▼* SFN** **♦EGSLL SYPILSCTAL ALLLLIVCC♦**
K RRYQQTLKQH TKVDPAFKPD LTGTSKSYVR SL

Fusion **▼ALLMOT15▼**

Peptide

▲107x178x4▲**▼.....EIGAI IGSVALGVA TAAQITAASA LIQANQNAAN ▲ILRLKESITA****TIEAVIIEVTDGLSQLAVA▲ VG KM▼ QQFVNDQFNNTAQELDCIKITQQV****▼ALLMOT15▼****GVELNLYLTELTTV FGPQITSPAL ▲TQLTIQALYNAGGNMDYLLTKLGVG****▲P1 & 12LZIPC▲****NNQLSSLIGSGLIT GN▼ ▲P1YDSQT QLLGIQVTLPSVGNLNNMRATYLET****LSVST TKGFASALVP KVVTQVGSVI EELDTSYCIE TDLDLYCTRI VTFPMSPGIY****SCLNGNTSAC MYSKTEGALT TPYMTLKGSV LANCKMTTCR CADPPGIISQ****▼ALLMOT15▼****▲107x178x4▲****NYGEAVSLID RHSCN ▲▼VSLSD GITLRLSGEF DATYQKNISI LDSQVITVG*****LVS Coiled-Coil******NLDISTELGNV NNSISNALDK LEESNSKLDK VNVKLTSTSA ▲▼Trans-****▼LIT* XIA****membrane Region****LTAISLVCGLSLV▼▲ LACYLMY▲ KQKAQQKTLWLGNNTLGQMRATTKM**

Fusion Peptide **FEFGGV** ♦ ALLMOTIS ♦
 ♦ 107x178x4 ♦ *LVS Coiled-Coil *
 ♦ IG ♦ TIALG ♦ VATSAQITAAVALVEAKQARS DIEKLKE

AIRDTNKAVOSVOSSSIGNLIVAIKSVQ* DYVNKE ♦ ♦ IVPSIARLGCEAAG

LQLGIALTQH ♦ ALLMOTIS ♦
 ♦ 107x178x4 ♦
 ♦ ♦ XSELTNIEGDNIGSLOEKGIKLOGIASLYRTNITE ♦ ♦

IFTTSTVDKYDIYDLLFTESIKVRVIDVDLNDYSITLQVRL ♦ P5 & 12LZIPC ♦
 ♦ PLLTRLLNTQIYR

VDSISYNI ♦ QNREWYI ♦ PLPSHIMTKG AFLGGADVKECIEAFSSYIC

PSDPGFVLNHEMESCLSGNISQCPRTVVKS DIVPRYAFVNGGVVANCITT

TCTCNGIGNRINQPPDQGVKIIHKECNTIGINGMLFNTNKEGTLAFYTP

NDITLNNSVALD ♦ P6 & 23LZIPC ♦
 ♦ PIDI ♦ SIELN ♦ KAKSDLEESKEWI ♦ RRSNQKL ♦

DSIGNWHOSSSTT ♦ Transmembrane Region ♦
 ♦ III ♦ LIM III IFINVT II ♦ ILAVKYY ♦ R
 IQKRN RVDQN DKPYVLTNK

Fusion
Peptide
.....GLEGAI AGFIENGWEGMIDGWYGFRHQNSEGTG

♦107x178x4♦

♦ALLMOTIS♦
LVS Coiled-Coil
*Q ♦AADLKST ♦QAAIDQINGKLNRYIEKTNEKEHQIEKEESEVEGRIQ

DLEKYVEDTKIDL* WSYNAELLVALENQHTI♦ DLT♦ DSEMNLFEKTR

RQLRENAEEMGNGCFKLYHKCDNACIESIRNGTYDHDVYRDEALNNRFQIKG

VELKSGYKDWLWISFAISCFLLCVVLLGFIMWACQRGNIRCNICL

FIG. 26

	Fusion Array		
	Purified	IC50 (X + T)	
	(up/ml)		
RSV F2	Y T S V I T E L S N I K C N G A K V K L I K Q E L D K Y K N A V T E L Q L L M A S T	RSV F2	AV
T-142	Y T S V I T E L S N I K C N G A K V K L I K Q E L D K Y K N	T-142	++
T-143	Y T S V I T E L S N I K C N G A K V K L I K Q E L D K Y K N	T-143	++
T-144	Y T S V I T E L S N I K C N G A K V K L I K Q E L D K Y K N A	T-144	+
T-145	Y T S V I T E L S N I K C N G A K V K L I K Q E L D K Y K N A V	T-145	++
T-146	Y T S V I T E L S N I K C N G A K V K L I K Q E L D K Y K N A V T	T-146	+
T-148	Y T S V I T E L S N I K C N G A K V K L I K Q E L D K Y K N A V T E	T-147	-
T-147	Y T S V I T E L S N I K C N G A K V K L I K Q E L D K Y K N A V T E L	T-148	-
T-149	Y T S V I T E L S N I K C N G A K V K L I K Q E L D K Y K N A V T E L Q	T-149	-
T-150	Y T S V I T E L S N I K C N G A K V K L I K Q E L D K Y K N A V T E L Q L	T-150	-
T-151	Y T S V I T E L S N I K C N G A K V K L I K Q E L D K Y K N A V T E L Q L L	T-151	+/+
T-152	Y T S V I T E L S N I K C N G A K V K L I K Q E L D K Y K N A V T E L Q L L M	T-152	+/+
T-153	Y T S V I T E L S N I K C N G A K V K L I K Q E L D K Y K N A V T E L Q L L M Q	T-153	-
T-154	Y T S V I T E L S N I K C N G A K V K L I K Q E L D K Y K N A V T E L Q L L M Q S	T-154	+/+
T-155	Y T S V I T E L S N I K C N G A K V K L I K Q E L D K Y K N A V T E L Q L L M Q S T	T-155	-

FIG. 27A

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RSV	Peptide #	AVG. IC50 (XTT) ug/ml
T-22	I E L L S N I K E N K C N G T D O A K Y K L I K Q E L D K Y K N A V T E L Q L L M Q S T	>500
T-23	I E L L S N I K E N K C N G T D O A K Y K L I K Q E L D K Y K N A V T E L Q L L M Q S T	>500
T-24	E N K C N G T D O A K Y K L I K Q E L D K Y K N A V T E L Q L L M Q S T	>500
T-25	D A K V K L I K Q E L D K Y K N A V T E L Q L L M Q S T	>500
T-26	C N Q T D A K V K L I K Q E L D K Y K N A V T E L Q L L M Q S T	>500
T-27	S N I K E N K C N G T D O A K V K L I K Q E L D K Y K N A V T E L Q L L M Q S T	>500
T-68	V S S K Q Y S A L R T Q W Y T S V I T I E L S N I K E N	165
T-334	A F I R K S D E I L L H N V	26
T-371	Y T S V I T I E L S N I K E N K U N G I D A K V K L I K Q E L D K Y K	>500
T-372	T S V I T I E L S N I K E N K U N G I D A K V K L I K Q E L D K Y K	NOT TESTED
T-373	S V I T I E L S N I K E N K U N G I D A K V K L I K Q E L D K Y K	>500
T-374	S N I K E N K U N G I D A K V K L I K Q E L D K Y K N A V T E L Q L L	>500
T-375	K E N K U N G I D A K V K L I K Q E L D K Y K N A V T E L Q L L M Q S	>500
T-575	A V S K Q Y L S A L R T Q W Y T S V I T I E L S N I K E N K U N G I D A	>100

F I 6. 27 B

RSV DP-107-LIKE REGION (F1)		Fusion Assay	
		RSV	PermEd
		(C10 X 77)	CO
RSV			
F1-107	A S G V A V S K V L H L E Q E V N K I A L L S T N K A V V S L S N O V S V L T S K V L D L K N Y I D K O L L	F1-107	AV
T-120	A S G V A V S K V L H L E Q E V N K I A L L S T N K A V V S L S N O	T-120	204
T-121	A S G V A V S K V L H L E Q E V N K I A L L S T N K A V V S L S N O	T-121	-
T-122	A S G V A V S K V L H L E Q E V N K I A L L S T N K A V V S L S N O	T-122	354
T-123	G V A V S K V L H L E Q E V N K I A L L S T N K A V V S L S N O	T-123	347
T-124	A V S K V L H L E Q E V N K I A L L S T N K A V V S L S N O	T-124	-
T-125	V S K V L H L E Q E V N K I A L L S T N K A V V S L S N O	T-125	84
T-126	V S K V L H L E Q E V N K I A L L S T N K A V V S L S N O	T-126	+
T-127	V S K V L H L E Q E V N K I A L L S T N K A V V S L S N O	T-127	89
T-128	V U L H L E Q E V N K I A L L S T N K A V V S L S N O	T-128	-
T-129	V U L H L E Q E V N K I A L L S T N K A V V S L S N O	T-129	343
T-130	H L E Q E V N K I A L L S T N K A V V S L S N O	T-130	-
T-131	H L E Q E V N K I A L L S T N K A V V S L S N O	T-131	41
T-132	L E Q E V N K I A L L S T N K A V V S L S N O	T-132	272
T-133	L E Q E V N K I A L L S T N K A V V S L S N O	T-133	307
T-134	G E V N K I A L L S T N K A V V S L S N O	T-134	41
T-135	G E V N K I A L L S T N K A V V S L S N O	T-135	187
T-136	G E V N K I A L L S T N K A V V S L S N O	T-136	60
T-137	N K I A L L S T N K A V V S L S N O	T-137	194
T-138	N K I A L L S T N K A V V S L S N O	T-138	99
T-139	N K I A L L S T N K A V V S L S N O	T-139	38
T-140	N K I A L L S T N K A V V S L S N O	T-140	86
T-141	N K I A L L S T N K A V V S L S N O	T-141	41
			204

Fig. 27 C

RSV	Pepptide #	AVG. IC50 (KTT) ug/m
T-12		
T-13		
T-15	V L H L E G E V N K I K S A L L S T N K A V V S L S N Q V S V L T S K V L D L K N Y I D K Q L L	>500
T-19		
T-28	A 8 Q V A V S K V L H L E G E V N K I K S A L L S T N K A V V S L S N Q V S V L T S K V L D L K N Y I D K Q L L	>500
T-29	8 Q V A V S K V L H L E G E V N K I K S A L L S T N K A V V S L S N Q V S V L T S K V L D L K N Y I D K Q L L	>500
T-30	V L H L E G E V N K I K S A L L S T N K A V V S L S N Q V S V L T S K V L D L K N Y I D K Q L L	>500
T-68	V V 8 L S N G V S V L T S K V L D L K N Y I D K Q L L	328
T-70	V N K I K S A L L S T N K A V V S L S N Q V S V L T S K V L D L K N Y I D K Q L L	292
T-66	N D Q K K L M S N N V Q I V R Q A S Y S I M S I I K E E	349
T-576	I 8 N I E T V I E F Q Q K N R L L E I T R E F S V N A Q V T T P V S	>100

FIG. 27 D

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RSV DP-178-LIKE REGION (F1)		Function	Amplitude	Purified
RSV				IC50
T-67		DEF DASI	SVNEKINQSLAFIRKSDELLHNVNA	(0.7mV) (XTT)
FI-178		GEP I INFYDPLVFP	SVNEKINQSLAFIRKSDELLHNVNA	CO
T-104		DEF DASI	SVNEKINQSLAFIRKSDELLHNVNA	+/-
T-105		DEF DASI	SVNEKINQSLAFIRKSDELLHNVNA	
T-106		DEF DASI	SVNEKINQSLAFIRKSDELLHNVNA	
T-107		DEF DASI	SVNEKINQSLAFIRKSDELLHNVNA	
T-108		DEF DASI	SVNEKINQSLAFIRKSDELLHNVNA	
T-109		DEF DASI	SVNEKINQSLAFIRKSDELLHNVNA	
T-110		DEF DASI	SVNEKINQSLAFIRKSDELLHNVNA	
T-111		DEF DASI	SVNEKINQSLAFIRKSDELLHNVNA	
T-112		DEF DASI	SVNEKINQSLAFIRKSDELLHNVNA	
T-113		DEF DASI	SVNEKINQSLAFIRKSDELLHNVNA	
T-114		DEF DASI	SVNEKINQSLAFIRKSDELLHNVNA	
T-115		DEF DASI	SVNEKINQSLAFIRKSDELLHNVNA	
T-116		DEF DASI	SVNEKINQSLAFIRKSDELLHNVNA	
T-117	(1-5741e)	DEF DASI	SVNEKINQSLAFIRKSDELLHNVNA	
T-118		DEF DASI	SVNEKINQSLAFIRKSDELLHNVNA	
T-119		DEF DASI	SVNEKINQSLAFIRKSDELLHNVNA	

FIG. 28A

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RSV	Pep tide #	AVG. IC50 (XTT) ug/ml
T-1	P I N F Y D P L V F P S D E F D A S I S Q V N E K I N Q S L A F I R	138

T-384 R M K Q A L E D K V E E I L S K L A F I R K S D E L L H N V

NOT TESTED

T-613	D E L L H N V N A Q K S T	>100
T-614	K S D E L L H N V N A Q K S T	>100
T-615	I R K S D E L L H N V N A Q K S T	>100
T-616	A F I R K S D E L L H N V N A Q K S T	>100
T-617 f	D A S I S Q V N E K I N Q S L A F I	NOT TESTED
T-682 s	L A F I R K S D E L L H N V N A Q K S T	>100
T-683 f	D A S I S Q V N E K I N Q S L A F I R K	NOT TESTED
T-685 f	D A S I S Q V N E K I N Q S L A F I R K S D E L L H N V N A Q K	7
T-686 f	D A S I S Q V N E K I N Q S L A F I R K S D E L L H N V N A	4
T-687 f	D A S I S Q V N E K I N Q S L A F I R K S D E L L H N V	4
T-688 f	D A S I S Q V N E K I N Q S L A F I R K S D E L L H	5
T-689 f	D A S I S Q V N E K I N Q S L A F I R K S D E L L	80
T-690 f	D A S I S Q V N E K I N Q S L A F I R K S D	>100
T-671 a	S I S Q V N E K I N Q S L A F I R K S D E L L H N V N A Q K S T	8
T-672	I S Q V N E K I N Q S L A F I R K S D E L L H N V N A Q K S T	6
T-673	S Q V N E K I N Q S L A F I R K S D E L L H N V N A Q K S T	14
T-674	N E K I N Q S L A F I R K S D E L L H N V N A Q K S T	>100
T-675	K I N Q S L A F I R K S D E L L H N V N A Q K S T	>100
T-678	N Q S L A F I R K S D E L L H N V N A Q K S T	>100
T-730 f	D A S I S Q V N E K I N Q S L A F I R K S D E L L H N V N A Q K S T	NOT TESTED

F I 6. 2 8 3

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HPV3 DP107-LIKE REGION (F1)		[C60] (pmol)	AV (pmol)
HPF107	071	167	167
157	ALQVATSAQITAAVVALVEAKQARSDIEKLKEAIROD	168	146*
158	ALQVATSAQITAAVVALVEAKQARSDIEKLKEAIROD	135	207*
159	QVATSAQITAAVVALVEAKQARSDIEKLKEAIROD	110	516*
160	YATSAQITAAVVALVEAKQARSDIEKLKEAIROD	141	190*
161	ATSAQITAAVVALVEAKQARSDIEKLKEAIROD	182	401*
162	TSQITAAVVALVEAKQARSDIEKLKEAIROD	183	121*
163	SAQITAAVVALVEAKQARSDIEKLKEAIROD	184	512,057*
164	QITAAVVALVEAKQARSDIEKLKEAIROD	185	742*
165	QITAAVVALVEAKQARSDIEKLKEAIROD	186	540*
166	ITAAVVALVEAKQARSDIEKLKEAIROD	187	215*
167	TAAVVALVEAKQARSDIEKLKEAIROD	188	680*
168	TAAVVALVEAKQARSDIEKLKEAIROD	189	137*
169	TAAVVALVEAKQARSDIEKLKEAIROD	170	456*
170	TAAVVALVEAKQARSDIEKLKEAIROD	171	417*
171	TAAVVALVEAKQARSDIEKLKEAIROD	172	47*
172	TAAVVALVEAKQARSDIEKLKEAIROD	173	50*
173	TAAVVALVEAKQARSDIEKLKEAIROD	174	56*
174	TAAVVALVEAKQARSDIEKLKEAIROD	175	56*
175	TAAVVALVEAKQARSDIEKLKEAIROD	176	740
176	TAAVVALVEAKQARSDIEKLKEAIROD	177	110*
177	TAAVVALVEAKQARSDIEKLKEAIROD	178	197,15
178	TAAVVALVEAKQARSDIEKLKEAIROD	179	150*
179	TAAVVALVEAKQARSDIEKLKEAIROD	180	205*
180	TAAVVALVEAKQARSDIEKLKEAIROD	181	712*
181	TAAVVALVEAKQARSDIEKLKEAIROD	182	929*
182	TAAVVALVEAKQARSDIEKLKEAIROD	183	707*
183	TAAVVALVEAKQARSDIEKLKEAIROD	184	218,50*
184	KEAIROD	185	67,8***
185	KEAIROD	186	542*
186	KEAIROD	187	613*
187	KEAIROD	188	152*
188	KEAIROD	189	669*

FIG. 29A

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Fig. 30A

T-268 (uncalibrated 201	457.500 $\mu\text{g}/\text{ml}$
T-428 205 mutant	101.61 $\mu\text{g}/\text{ml}$
T-363 R M K Q L E D K V E E L L S K L E W I R R S N Q K L D S I	NOT DONE
T-577 O Q I K Q A Y K R L L D R L I P L Y D Q L R Q K O V I V S N Q E S N	133.793 $\mu\text{g}/\text{ml}$
T-578 Y S E L T N I F Q D N I Q S L O E K O I K L O Q I A S L Y R T N I T E I	107.177 $\mu\text{g}/\text{ml}$
T-579 T S I T L Q V R L P L L T R L L N T Q I Y R V D S I S Y M I O N R E W Y	NOT DONE

F 26. 30 B

Fusion

♥ALLMOT15♥

Peptide

♦107x178x4♦

.....RNKRGVFVLGFLGFLATAGSAMGAAS ♦♥ XXXXAQSRTLLAGIVQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKYLKDQAQL♦NAWG♥ CAF

♥ALLMOT15♥

*LVS Predicted Coiled-Coil

RQVCHTTVPWPNAASLTPDW *NND ♥ TWQEWERKVDFLEENITALLEEAQIQQ

♦107x178x4♦

EKNMY ♦ELQKLNSWD* VF♥ GNXXXXXXXXXXXXXXXXXXXXXX♦

IYIVMLAKLRQGYRPVFSSPPSYFQXTHTQQDPALPTREGKEGDGGEGGGNSSWP

WQIEYIHF

FIG. 31

MTRRRVLSVVVLLAALACRLGAQTPEQPAPPATTVQPTATRQQTSFPFRVCELSHGDLFRFSSD

▲107x178x4▲

IQCPSFGTRENHTEGLLMVFKDNIIPYSF ▲KVRSYTKIVTNILYNGWYADSVTNRHE▲

EKFSVDSY ETDQMDTIYQ CYNAVKMTKD GLTRVYVDRD GVINITVNLKP TGGLANGVRR

YASQTELYDA PGWLIWTYRT RTTVNCLITD MMAKSNSPFD FFVTTGQTV EMSPFYDGKN

KETFHERADS FHVRTNYKIV DYDNRGTPNPQ GERRAFLDKG TYTLSWKLEN RTAYCPLQHW

QTFDSTIATE TGKSIHFVTD EGTSSFVTNT TVGIELPDAF KCIEEQVNKT HEKYEAVQD

RYTKGQEAIT YFITSGLLL AWLPLTPRSL ATVKNLTELT TPTSSPPSSP SPPAPSAARG

STPAAVLRRR RRDAGNATTVP VPPTAPGKSL GTLNNPATVQ IQFAYDSLRR QINRMLGDLA

RAWCLEQKRQ NMVLRELTGIA NPTTVMSSIY GKAVALAKRLG DVISVSQCVP VNQATVTLRK

SMRVPGSETM CYSRPLVSFS FINDTKTYEG QLGTDNEIFL TKKMTEVCQA TSQYYFQSGN

▲107x178x4▲

EIHVYNDYHH FKTIELDGIA TLQTFISLNT ▲SLIENIDFASLELYSRDEQRASNVD *LE▲

LVS Predicted Coiled Coil

TM Potential

GIFREYNFQAQNIAGLRKDLDNAVSN* GRNQ FVDGLGELMDSLGSVG QSITN

•P12LZIPC•

TM Potential

TM Potential
LVSTVGGLFSSLVSGFISFKN •PFGGMLILVLVAGVVILVISL• TRRTRQMS

QQPVQMLYPG IDELAQQHAS GEGPGINPIS KTELQAIMLA LHEQNQEQRK AAQRAAGPSV

ASRALQAARDRFPGLRRRY HDPETAAALL GEAETEF

FIG. 32

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MMDPNSTSED VKFTPDPYQV PFVQAFDQAT RVYQDLGGPS QAPLPCVLWP VLPEPLPQQGQ

LTAYHVSTAP TGSWFSAPQP APENAYQAYA APQLFPVSDI TQNQQTNQAG GEAPQPGDNS

TVQTAAAVVF ACPGANQGQQ LADIGVPQPA PVAAPARRTR KPQQPESLEE CDSELEI

@DNA Binding@ ▲107x178x4▲ +Dimerization+
@KRY KNRVASRKCRAK ▲FK@ Q +LLQHYREVAAAKSSENDRLRLLLKQ▲

MCPSLDVD+ SI IPRTPDVLHE DLLNF

FIG. 33

7872-020 (SHEET 41 OF 63)

Fusion
Peptide
FAG

♥ ALLMOTIS ♥
♥ VVLAGAALGVATAAQITAGIALHQSM *

LVS Coiled-Coil
NSQAIIDLNRASLETTN

QAIEAIRQAGQEMI *LAVQGVQDYTNN ♥ ELIPSMNQLSCDLIGQKLGLKLLRYYT

♦ P23LZIPC ♦

♦ P6,12LZIPC ♦

♦ 107x178x4 ♦

♥ ALLMOTIS ♥

EILSLFGPSLRD ♦ PISA ♦ ♥ EISIQALSYALGGDINKV ♦ LEKLGYSGGDL ♦

♦ P1,12LZIPC ♦

LGILES ♦ RGIKARI ♥ THVDTESYFIVLSIAY ♦ PTLSEIKGVIVHRLEGV ♦ SY

NIGSQEWYTTVPKYVATQGYLISNFDESSCTFMPEGTVCSQNAL YPMSPLLQECL

RGSTKSCARTLVSGSFGNRFILSQGNLIANCASILCKCYTTGTIINQDPDKILTYIAA

♦ P23LZIPC ♦

♦ P12LZIPC ♦

♥ ALLMOTIS ♥

LVS Coiled-Coil

DHCPVVEVNGVTIQVGSRRYPDAVYLHRIDLGP ♦ P ♥ IS *LERLDVGTNLGN

♦ Transmembrane Region ♦

AIAKLEDAKELL ♦ ESSDQI *L ♦ RSMK ♦ GLSSTSIVYILI ♥ AVCLGGGLIGIP

ALICCC ♦ RGRCNKKGEQVGMSRPGLKPDLTGTSKSYVRSL

FIG. 34

Pre S1 and Pre S2

MGQNLSTS NPLGFFPDHQ LDPAFRANTANPDWDFNPNKDTWPDANKVGAGAFG
LGFTPPHGGLLGWSPQAQGILQTL PANPPPASTNRQSGRQPTPLS PPLRNTHPQAM
QWNSTTFHQTLQDPRVRGLYFPAGGSSSGTVNPVLTASPLSSIFS RIGDPALN

Major Surface Antigen (HBs)

Fusion

Peptide

♦P12 & 23LZIPC♦

MENITSG FLG ♦PLL VLQAGFFLLTRILTI♦ PQSLDSWWTSLNFLGGTTVCLG

♦P12 & 23LZIPC♦

QNSQSPTSNHSPTSCPPTC ♦PGYRW MCLRRFIIFL FILLLCLIFLLVLLDYQGML♦

PVCPLIPGSSTTSTGPCRTCM TTAQGTSMYPSCCCTKPSDGNCTCIPSSWAFGKF

♦Transmembrane Region♦LWEWASARFSWLS ♦LLVPFVQWFVGLSPTVWLSVI♦ WMMWYWGPSL♦Transmembrane Region♦♦YSILSPFLPLLPIFFCLWVYI♦

FIG. 35

Fusion
Peptide

♥ ALLMOTIS ♥

▲ 107x178x4 ▲

*LVS Coiled Coil

AIQLIPLFVG LGI ♥ TTAVSTGAAGLGVS ▲ IT *QYTKLSHQLISDV

QAISSTIQDLQDQVDSLAEVVLQ* NRRGLDLLTAE ▲ QGGI ♥

CLALQEKCCFYANKSGIVRDKIKNLQDDLERRRQLIDNPFWTSFHG

FLPYVMPLLGPLLCLLLVLSFGPIIFNKLMTFIKHQIESIQAKPIQVHYH

Transmembrane Region

RLEQEDSGGSYLTLT.....????????????????????????????.....

FIG 36

MKAQKGFTLI ELMIVVVAIIG ILAAIAIPQ

♦ 107x178x4 ♦

♥ ALLMOTI5 ♥

♦ ♥ YQDYTARTQVTRAVSEVSALKTAAESAILEGKEIVSSA ♦ T ♥

PK DTQYDIGFT

♦ 107x178x4 ♦

♥ ALLMOTI5 ♥

♦ ♥ ESTLLDGSGKSQIQVTDNQDGTVELVATLGKSSGS ♦ AIKGAVITVSR ♥

KNDGV WNCKITKTPT AWKPNYAPAN CPKS

FIG. 37

MNTLQKGFTL IELMIVIAIV GILAAVALPA YQDYTARAQV

SEAILLAEGQ KSAVTEYYLN HGIWP

♦ 107x178x4 ♦
♥ ALLMOTI5 ♥
♦ ♥ KDNTSAGVASSSIKGKYVKEVKVENGVVTAT ♦

MNSSNVNKEIQGKKLSLWAKRQDGSVKW ♥

FCGQP VTRNAKDDTV TADATGNDGK IDTKHLPSTC RDNFDAS

FIG. 38

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MKKTLLGSLI LLAFAGNVQA DINTETSGKV TFFGKVVENT

CKVKTEHKNL SVVLNDVGKN SLSTKVNTAM PTPFTITLQN

CDPTTANGTA NKANKVGLYF Y

▲107x178x4▲
♥ALLMOTI5♥
▲♥SWKNVDKENNFTLKNEQTTADYATNVNI▲

QLMESNGTKAISVVGKETE♥

DF MHTNNNGVAL NQTHPNNAHI SGSTQLTTGT NELPLHFIAQ

YYATNKATAG KVQSSVDFQI AYE

FIG. 39

MNKKLLMNFF IVSPLLATT ATDFTPVP

♦107x178x4♦

♥ALLMOT15♥

♦♥LSSNQIIKTAKASTNDNIKDLLDWYSSGSDTFTNS♦♥

EVLDNSL GSMRIKNTDG SISLIIFPSP YYSPAFTKGE KV

♦107x178x4♦

♦DLNTKRTKKSQHTSEGTYIHFQISGVT♦

N TEKLPTPIEL PLKVKVHGKD SPLKYG

♦P12LZIPC♦

♦PKFDKKQLAISTLDFEIRHQLTQI♦

HGLYRSSDKT GGYWKITMND GSTYQSDL SK KFEYNTEKPP

INIDEIKTIE AEIN

FIG. 40

♥ALLMOT15♥

MKKTAFILLI FIALTLLTSP L ♥VNG

♦107x178x4♦

LVS Predicted Coiled-Coil

S ♦EKSEEINEKDLRKKSELQRNALSNLRQIY YYNEKAITENKESDD♦

QFLENTLL♥ FKG FFTGHPW

♦107x178x4♦

♦YNDLLVDLGSKD ATNKYKGKKVDLYGAY♦

YGYQCAGGTPNKTACMYGGVTLHDN NRLTEEKV P INLWIDGKQTTV

♦P12LZIPC♦

♦PIDKVKT SKKEVTVQELDL♦ QARHYLHGK FGLYNSDSFGGKVQ

♦P12LZIPC♦

RGLIVF HSSEGSTVSY DLFDAQGQY ♦P DTLLRIYRDN KTINSEN LHI♦

DLYLYTT

FIG. 41

♥ALLMOTI5♥

♥VNNGS

MKKTAFTLLL FIALTLLTSP L

♦107x178x4♦

♦EKSEEINEKDLRKKSELQGTALGNLKQIYYYNEAKTENKESHD♦ Q♥

FLQHTILFKG FFTDHSWYND LLVDFDSKDI VDKYKGKKVDLYGAYY

GYQC AGGTPNKTAC MYGGVTLHDN NRLTEEKVPINL WLDGKQNTV

♦107x178x4♦

♥ALLMOTI5♥

♦P12LZIPC♦

♦P ♥L ♦ETVKTNKKNVTVQELDLQARRYL♦ QEKYNLYN♦

SDVFDGKVQR♥ GLIVF HTSTE

♦P23LZIPC♦

♦PSVNYDLFGAQGQYSNTLLRIYRDNKTINSENMHI♦ DIYLYTS

FIG. 42

MKNITFIFFILLASPLYANGDRLYRADSRRPDEIKRFRSLMPRGNEYFDRGT

♥ALLMOTIS♥

♥QMNINLYDHARGTQTGFVRYDDGYV

♦107x178x4♦

♦STSLSLRSAHLAGQYILSGYSLTIYVI♦ ANMFNVNDVISVY♥

SP HPYEQEVSAL GGIPYSQIYG WYRVNFGVID ERLHRNREYR

DRYYRNLNIA PAEDGYRLAG FPPDHQA WRE EPWIHHAPQG

CGDSSRTITG DTCNE

♥ALLMOTIS♥

♥ETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL♥

FIG. 43

MMFSEGFnADY EASSSRCSSA SPAGDSLSYY HSPADSFSSM

GSPVNAQDFC TDLAVSSANF IPTVTAISTS PDLQWLVQPA

LVSSVAPSQT RAPHFGVPA PSAGAYSRAG VVKTMTGGRA

LVS Predicted Coiled-Coil

QSIGRRGKVE QLSPEEEEKR RIRRE *RNKMA AAK

♦107x178x4♦

♥ALLMOTI5♥

♥CRNRRREL ♦TDTLQAETDQLEDEKSALQTEIANLLKEKEKL♦♥

EFILAAH R* PACKIPDDL GFPEEMSVAS LDLTGGLPEV

ATPEEEAFT LPLLNDPEPK PSVEPVKSIS SMELKTEPFD

DFLFPASSRP SGSETARSVP DMDLSGSFYA LPLLNDPEPK

PSVEPVKSIS SMELKTEPFD DFLFPASSRP SGSETARSVP

DMDLSGSFYA GSSSNEPSSD SLSSPTLLAL

FIG. 44

SGWESYYKTEGDEEAEEEQEEENLEASGDYKYSGRDSLIFLVDASKA
MFESQSEDELTPFDMSIQCIQSYYISKISSLDRDLLAVVFYGTKEKDKNS
VNFKNITYVLQELDNPGAKRILELDQFKGQQGQKRFQDMMGHGSDY
SLSEVLWVCANLFSDVQFKMSHKRIMLFTNEDNPHGNDSAKRASRAR
TKAGDLRDTGIFLDLMHLKKPGGFDISLFYRDIISIAEDED

▲107x178x4▲

♥ALLMOTI5♥

LVS Predicted Coiled-Coil

♥LRVH *FEE ♠SSKLEDLLRKVRAKETRKRALSRKLKLNKDIV* ISV

GIYNLVQKAL♥ KPPPIKLYRETN♠ EPVKTTRTFNTSTGGLLLPSDTKR

SQIYGSRQIILEKEETEELKRFDDPGLMLMGFKPLVLLKKHHLRPSLFVYPE
ESLVIGSSTLFSALLIKCLEKEVAALCRYTPRRNIPPYFVALVPQEEELDDQK
IQVTPPGFQLVFLPFADDKRKMPFTEKIMATPEQVGKMKAIIVEKLRFTYRS
DSFENPVLQQHFRNLEALALDLME

♦P12LZIPC♦

♦PEQAVDLTPKVEAMNKRL♦ GSLVDEFKELVYPPDYNPEGKVTKR
KHDNEGSGSKRPKVEYSEEELKTHISKGTGKFTVPMLEACRAYGLKSG
LKKQELLEALTKHFQD

FIG. 45

GGGALSPQHSAVTQGSIIKNKEGMDAKS

♦107x178x4♦

♥ALLMOT15♥

♥♦LTAWSRTLVTFKDVFVDFTREEWKLLDT♦ AQQIVYRNV

MLENYKNLVSLGYQLT♥ KPDVILRLEKGEWPWLVEREIHQETHPD
SETAFEIKSSVSSRSIFKDKQSCDIKMEGMARNDLWYLSLEEVWKCR
DQLDKYQENPERHLRHQLIHTGEKPYECKEKGKSFSRSSHLIGHQKT
HTGEEPYECKEKGKSFSWFSLVTHQRTHGDLYTCNQCGKSFVH
SSRLIRHQRTHGTGHKPYECPECGKSFRQSTHLILHQRTHVRVRPYECN
ECGKSYSQRSHLVVHHRIHTGLKPFECKDCGKCFSRSSHLYSHQRTH
TGEKPYECHDCGKSFSQSSALIVHQRIHTGEKPYECCQCGKAFIRKN
DLIKHQRIHVGAETYKCNQCGIIFSQNS

♦P23LZIPC♦

♦PFIVHQIAHTGEQFLTCNQCGTALVNTSNLIGYQTNHI♦ RENAY

FIG. 46

Fig. 47

Simian Immunodeficiency Virus Mm251												Antiviral Activity	
DP178-like		Residue										SIV	
Residue	245	246	247	248	249	250	251	252	253	254	255	47	
T-390	245	T	W	Q	E	W	E	R	K	V	D	F	LEENITALL
T-391	246	T	W	Q	E	W	E	R	K	V	D	F	LEENITALL
T-392	247	T	Q	E	W	E	R	K	V	D	F	LEENITALL	
T-393	248	E	W	E	R	K	V	D	F	LEENITALL	E	Q	EEKQALKL
T-394	249	W	E	R	K	V	D	F	LEENITALL	E	Q	Q	EEKQALKL
T-395	250	E	R	K	V	D	F	LEENITALL	E	Q	Q	Q	EEKQALKL
T-396	251	R	K	V	D	F	LEENITALL	E	Q	Q	Q	Q	EEKQALKL
T-397	252		K	V	D	F	LEENITALL	E	Q	Q	Q	Q	EEKQALKL
T-398	253		V	O	F	L	E	E	N	I	T	Q	EEKQALKL
T-399	254		D	F	L	E	E	A	Q	Q	E	K	EEKQALKL
T-400	255		F	L	E	E	A	Q	Q	E	K	N	EEKQALKL

Fig. 48

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HIV-1 Bpu 178 Constructs, Mutations		HIV-1/Bpu		HIV-1/Bpu	
Pl	Removed Mutants Added	IC50 (nM)	IC50 (nM)	IC50 (nM)	IC50 (nM)
T695	X	AA	AA	AA	AA
T574	X	C 0 0 Y	C 0 0 Y	C 0 0 Y	C 0 0 Y
T580	X	C13H27CO-	C13H27CO-	C13H27CO-	C13H27CO-
T573	X	Free Termin	No Ac-	Y T B L I H S L I E E S	Y T B L I H S L I E E S
T64	X	Dig-	Dig-	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T83	X	Biotin-	Biotin-	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T708	X	Biotin-NHCH2)8CO-	Biotin-NHCH2)8CO-	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T707	X	Biotin-NHCH2)4CO-	Biotin-NHCH2)4CO-	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T20		Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T95	X	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T98	X	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T97	X	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T98	X	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T99	X	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T103	X	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T212	X	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T213	X	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T214	X	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T215	X	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T216	X	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T229	X	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T230	X	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T231	X	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T379	X	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T701	X	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T702	X	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T703	X	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T704	X	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T705	X	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T706	X	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T158	X	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T89	X	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S
T90	X	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S	Y T S L I H S L I E E S

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Fig. 50.

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Residue	187	L Q H Y R E V A A A K S S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D	242	46
T-447	187	L Q H Y R E V A A A K S S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D	232	36
T-448	188	Q H Y R E V A A A K S S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D	233	36
T-449	189	H Y R E V A A A K S S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D	234	36
#	200	Y R E V A A A K S S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D	236	36
T-451	201	R E V A A A K S S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D	238	36
T-452	202	E V A A A K S S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D	237	36
T-453	203	V A A A K S S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D	238	36
T-454	204	A A A K S S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D	239	36
T-455	205	A A K S S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D	240	36
T-456	206	A K S S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D	241	36
T-457	207	K S S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D	242	36
T-458	208	S S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D	243	36

Residue	209	S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D L L N F	248	37
T-459	209	S E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D L L N F	244	36
T-460	210	E N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D L L N F	246	36
T-461	211	N D R L R L L K Q M C P S L D V D S I I P R T P D V L H E D L L N F	246	36

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Domain I:

174P-L-L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-G-T-T-V-C-L-G-Q-N-S-Q-S-P220

P-L-L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T
L-L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V
L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V
V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C
L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L
Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G
A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q
G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N
F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S
F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S-Q
L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S-Q-S

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Domain II:
223P-G-Y-R-W-M-C-L-R-R-F-I-I-F-L-F-I-L-L-C-L-I-F-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I-P-G-S-S-T-G-P-C-R-T-C-M-T-T291

P-G-Y-R-H-M-C-L-R-R-F-I-I-F-L-F-I-L-L-C-L-I-F-L-V-L-L-D-Y-Q-G-M-L
 Q-Y-R-W-M-C-L-R-R-F-I-I-F-L-F-I-L-L-C-L-I-F-L-V-L-L-D-Y-Q-G-M-L-P
 Y-R-W-M-C-L-R-R-F-I-I-F-L-F-I-L-L-C-L-I-F-L-V-L-L-D-Y-Q-G-M-L-P-V
 R-W-M-C-L-R-R-F-I-I-F-L-F-I-L-F-L-F-I-L-L-C-L-I-F-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P
 W-M-C-L-R-R-F-I-I-F-L-F-I-L-F-L-F-I-L-L-C-L-I-F-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L
 M-C-L-R-R-F-I-I-F-L-F-I-L-F-L-F-I-L-L-C-L-I-F-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L
 C-L-R-R-F-I-I-F-L-F-I-L-F-L-F-I-L-L-C-L-I-F-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-U-I
 U-R-R-F-I-I-F-L-F-I-L-L-C-L-I-F-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-U-I-P
 R-R-F-I-I-F-L-F-I-L-L-C-L-I-F-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-U-I-P-Q
 R-F-I-I-F-L-F-I-L-L-C-L-I-F-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-U-I-P-Q-S
 P-I-I-F-L-F-I-L-L-C-L-I-F-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-U-I-P-G-S-S
 I-I-F-L-F-I-L-L-C-L-I-F-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-U-I-P-G-S-S-T
 I-F-L-F-I-L-L-C-L-I-F-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I-P-G-S-S-T-S
 P-L-F-I-L-L-C-L-I-F-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I-P-G-S-S-T-S-T
 L-F-I-L-L-C-L-I-F-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I-P-G-S-S-T-S-T-Q
 F-I-L-L-C-L-I-F-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I-P-G-S-S-T-S-T-Q-P
 I-L-L-C-L-I-F-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I-P-G-S-S-T-S-T-Q-P-C
 U-L-L-C-L-I-F-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I-P-G-S-S-T-S-T-Q-P-C-R
 L-L-C-L-I-F-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I-P-G-S-S-T-S-T-Q-P-C-R-T
 L-C-L-I-F-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I-P-G-S-S-T-S-T-Q-P-C-R-T-C
 C-L-I-F-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I-P-G-S-S-T-S-T-Q-P-C-R-T-C-M
 L-I-F-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I-P-G-S-S-T-S-T-Q-P-C-R-T-C-M-T
 I-F-L-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I-P-G-S-S-T-S-T-Q-P-C-R-T-C-M-T

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